



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: C12N 15/12, C07K 14/47, C12N 16/70, 1/21, A61K 38/17, C07K 16/18, C12Q 1/68	A2	(11) International Publication Number: WO 99/15658 (43) International Publication Date: 1 April 1999 (01.04.99)
(21) International Application Number: PCT/US98/19839 (22) International Filing Date: 22 September 1998 (22.09.98) (30) Priority Data: 08/933,750 23 September 1997 (23.09.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 08/933,750 (CIP) Filed on 23 September 1997 (23.09.97) (71) Applicant (for all designated States except US): INCYTE PHARMACEUTICALS, INC. [US/US]; 3174 Porter Drive, Palo Alto, CA 94304 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LAL, Preeti [IN/US]; 2382 Lass Drive, Santa Clara, CA 95054 (US). HILLMAN, Jennifer, L. [US/US]; 230 Monroe Drive #12, Mountain View, CA 94040 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Mountain View, CA 94043 (US). SHAH, Purvi [IN/US]; 1608 Queen Charlotte Drive #5, Sunnyvale, CA 94087 (US). AU-YOUNG, Janice [US/US]; 1419 Kains	Avenue, Berkeley, CA 94702 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). GUEGLER, Karl, J. [CH/US]; 1048 Oakland Avenue, Menlo Park, CA 94025 (US). (74) Agents: BILLINGS, Lucy, J. et al.; Incyte Pharmaceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: HUMAN REGULATORY MOLECULES (57) Abstract <p>The invention provides human regulatory molecules and polynucleotides (collectively designated HRM) which identify and encode them. The invention also provides expression vectors, host cells, agonists, antibodies and antagonists. The invention further provides methods for diagnosing, preventing, and treating disorders associated with expression of human regulatory molecules.</p>		

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HUMAN REGULATORY MOLECULES

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TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human regulatory molecules which are important in disease and to the use of these sequences in the diagnosis, prevention, and treatment of diseases associated with cell proliferation.

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BACKGROUND OF THE INVENTION

Cells grow and differentiate, carry out their structural or metabolic roles, participate in organismal development, and respond to their environment by altering their gene expression. Cellular functions are controlled by the timing and amount of expression attributable to thousands of individual genes. The regulation of expression is metabolically vital in that it
15 conserves energy and prevents the synthesis and accumulation of intermediates such as RNA and incomplete or inactive proteins when the gene product is not needed.

Regulatory protein molecules are absolutely essential in the control of gene expression. These molecules turn individual or groups of genes on and off in response to various inductive mechanisms of the cell or organism; act as transcription factors by
20 determining whether or not transcription is initiated, enhanced, or repressed; and splice transcripts as dictated in a particular cell or tissue. Although regulatory molecules interact with short stretches of DNA scattered throughout the entire genome, most gene expression is regulated near the site at which transcription starts or within the open reading frame of the gene being expressed. The regulated stretches of the DNA can be simple and interact with
25 only a single protein, or they can require several proteins acting as part of a complex to order to regulate gene expression.

The double helix structure and repeated sequences of DNA create external features which can be recognized by the regulatory molecules. These external features are hydrogen bond donor and acceptor groups, hydrophobic patches, major and minor grooves, and regular,
30 repeated stretches of sequence which cause distinct bends in the helix. Such features provide recognition sites for the binding of regulatory proteins. Typically, these recognition sites are less than 20 nucleotides in length although multiple sites may be adjacent to each other and

each may exert control over a single gene. Hundreds of these DNA sequences have been identified, and each is recognized by a different protein or complex of proteins which carry out gene regulation.

The regulatory protein molecules or complexes recognize and bind to specific nucleotide sequences of upstream (5') nontranslated regions, which precede the first translated exon of the open reading frame (ORF); of intron junctions, which occur between the many exons of the OR; and of downstream (3') untranslated regions, which follow the ORF. The regulatory molecule surface features are extensively complementary to the surface features of the double helix. Even though each individual contact between the protein(s) and helix may be relatively weak (hydrogen bonds, ionic bonds, and/or hydrophobic interactions) and the 20 or more contacts occurring between the protein and DNA result in a highly specific and very strong interaction.

Families of regulatory molecules

Many of the regulatory molecules incorporate one of a set of DNA-binding structural motifs, each of which contains either α helices or β sheets and binds to the major groove of DNA. Seven of the structural motifs common to regulatory molecules are helix-turn-helix, homeodomains, zinc finger, steroid receptor, β sheets, leucine zipper, and helix-loop-helix.

The helix-turn-helix motif is constructed from two α helices connected by a short chain of amino acids, which constitutes the "turn". The two helices interact with each other to form a fixed angle. The more carboxy-terminal helix is called the recognition helix because it fits into the major groove of the DNA. The amino acid side chains of the helix recognize the specific DNA sequence to which the protein binds. The remaining structure varies a great deal among the regulatory proteins incorporating this motif. The helix-turn-helix configuration is not stable without the rest of the protein and will not bind to DNA without other peptide regions providing stability. Other peptide regions also interact with the DNA, increasing the number of unique sequences a helix-turn-helix can recognize.

Many sequence-specific DNA binding proteins actually bind as symmetric dimers to DNA sequences that are composed of two very similar half-sites, also arranged symmetrically. This configuration allows each protein monomer to interact in the same way with the DNA recognition site and doubles the number of contacts with the DNA. This doubling of contacts greatly increases the binding affinity while only doubling the free energy of the interaction. Helix-turn-helix motifs always bind to DNA that is in the B-DNA form.

The homeodomain motif is found in a special group of helix-turn-helix proteins that are encoded by homeotic selector genes, so called because the proteins encoded by these genes control developmental switches. For example, mutations in these genes cause one body part to be converted into another in the fruit fly, Drosophila. These genes have been found in every eukaryotic organism studied. The helix-turn-helix region of different homeodomains is always surrounded by the same structure, but not necessarily the same sequence, and the motif is always presented to DNA the same way. This helix-turn-helix configuration is stable by itself and, when isolated, can still bind to DNA. It may be significant that the helices in homeodomains are generally longer than the helices in most HLH regulatory proteins.

Portions of the motif which interact most directly with DNA differ among these two families. Detailed examples of DNA-protein binding are described in Pabo, C.O. and R.T. Sauer (1992; Ann. Rev. Biochem. 61:1053-95).

A third motif incorporates zinc molecules into the crucial portion of the protein. These proteins are most often referred to as having zinc fingers, although their structure can be one of several types. Proteins in this family often contain tandem repeats of the 30-residue zinc finger motif, including the sequence patterns Cys-X₂ or 4-Cys-X₁₂-His-X₃-5-His. Each of these regulatory proteins has an α helix and an antiparallel β sheet. Two histidines in the α helix and 2 cysteines near the turn in the β sheet interact with the zinc ion which holds the α helix and the β sheet together. Contact with the DNA is made by the arginine preceding the α helix, and by the second, third, and sixth residues of the α helix. When this arrangement is repeated as a cluster of several fingers, the α helix of each finger can contact and interact with the major groove of the DNA. By changing the number of zinc fingers, the specificity and strength of the binding interaction can be altered.

The steroid receptors are a family of intracellular proteins that include receptors for steroids, retinoids, vitamin D, thyroid hormones, and other important compounds. The DNA binding domain of these proteins contains about 70 residues, eight of which are conserved cysteines. The steroid receptor motif forms a structure in which two α helices are packed perpendicularly to each other, forming more of a globular shape than a finger. Each helix has a zinc ion which holds a peptide loop against the N-terminal end of the helix. The first helix fits into the major groove of DNA, and side chains make contacts with edges of the DNA base pairs. The steroid receptor proteins, like the helix-turn-helix proteins, form dimers that bind the DNA. The second helix of each monomer contacts the phosphate groups of the

DNA backbone and also provides the dimerization interface. In some cases, multiple choices can exist for heterodimerization which produces another mechanism for fine-tuning the regulation of numerous genes.

Another family of regulatory protein molecules uses a motif consisting of a two-stranded antiparallel β sheet to recognize the major groove of DNA. The exact DNA sequence recognized by the motif depends on the amino acid sequence in the β sheet from which the amino acid side chains extend and contact the DNA. In two prokaryotic examples of the β sheet, the regulatory proteins form tetramers when binding DNA.

The leucine zipper motif commonly forms dimers and has a 30-40 residue motif in which two α helices (one from each monomer) are joined to form a short coiled-coil. The helices are held together by interactions among hydrophobic amino acid side chains (often on heptad-repeated leucines) that extend from one side of each helix. Beyond this, the helices separate, and each basic region contacts the major groove of DNA. Proteins with the leucine zipper motif can also form either homodimers or heterodimers, thus extending the specific combinations available to activate or repress expression.

Yet another important motif is the helix-loop-helix, which consists of a short α helix connected by a loop to a longer α helix. The loop is flexible and allows the two helices to fold back against each other. The α helices bind both to DNA and to the HLH structure of another protein. The second protein can be the same (producing homodimers) or different (producing heterodimers). Some HLH monomers lack sufficient α helix to bind DNA, but they can still form heterodimers which can serve to inactivate specific regulatory proteins.

Hundreds of regulatory proteins have been identified to date, and more are being characterized in a wide variety of organisms. Most regulatory proteins have at least one of the common structural motifs for making contact with DNA, but several important regulatory proteins, such as the p53 tumor suppressor gene, do not share their structure with other known regulatory proteins. Variations on known motifs and new motifs have been and are currently being characterized (Faisst, S. and S. Meyer (1992) Nucl. Acids Res. 20: 3-26).

Although binding of DNA to a regulatory protein is very specific, there is no way to predict the exact DNA sequence to which a particular regulatory protein will bind or the primary structure of a regulatory protein for a specific DNA sequence. Thus, interactions of DNA and regulatory proteins are not limited to the motifs described above. Other domains of the proteins often form crucial contacts with the DNA, and accessory proteins can provide

important interactions which may convert a particular protein complex to an activator, or a repressor, or may prevent binding (Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing Co, New York NY, pp. 401-74).

Diseases and disorders related to gene regulation

- 5 Many neoplastic growths in humans can be traced to problems of gene regulation. Malignant growth of cells may be the result of excess transcriptional activator or loss of an inhibitor or suppressor (Cleary ML (1992) *Cancer Surv.* 15:89-104). Alternatively, gene fusion may produce chimeric loci with switched domains, such that the level of activation is no longer correct for the gene specificity of that factor.
- 10 The cellular response to infection or trauma is beneficial when gene expression is appropriate. However, when hyper-responsivity or another imbalance occurs for any reason, improper or insufficient regulation of gene expression may cause considerable tissue or organ damage. This damage is well documented in immunological responses to allergens, heart attack, stroke, and infections (Harrison's Principles of Internal Medicine, 13/eth, (1994)
- 15 McGraw Hill, Inc. and Teton Data Systems Software). In addition, the accumulation of somatic mutations and the increasing inability to regulate cellular responses is seen in the prevalence of osteoarthritis and onset of other disorders associated with aging.

The discovery of new human regulatory protein molecules which are important in disease development and the polynucleotides encoding them satisfies a need in the art by

20 providing new compositions which are useful in the diagnosis, prevention and treatment of diseases associated with cell proliferation, particularly immune responses and cancers.

SUMMARY OF THE INVENTION

The invention features substantially purified polypeptides, human regulatory molecules, collectively referred to as HRM and individually referred to as HRM-1 through

25 HRM-10, having at least one of the amino acid sequences selected from the group consisting of SEQ ID NOs:1-10.

The invention further provides isolated and substantially purified polynucleotide sequences encoding HRM. In a particular aspect, the polynucleotide is at least one the nucleotide sequences selected from the group consisting of SEQ ID NOs:11-20.

30 In addition, the invention provides a polynucleotide sequence, or fragment thereof, which hybridizes under stringent conditions to any of the polynucleotide sequences of SEQ ID NOs:11-20. In another aspect the invention provides compositions comprising isolated

and purified polynucleotide sequences of SEQ ID NOs:11-20 or fragments thereof.

The invention further provides a polynucleotide sequence comprising the complement or fragments thereof of any one of the polynucleotide sequences encoding HRM. In another aspect the invention provides compositions comprising isolated and purified polynucleotide
5 sequences comprising the complements of SEQ ID NOs:11-20 or fragments thereof.

The present invention further provides an expression vector containing at least a fragment of any one of the polynucleotide sequences of SEQ ID NOs:11-20. In yet another aspect, the expression vector containing the polynucleotide sequence is contained within a host cell.

10 The invention also provides a method for producing a polypeptide or a fragment thereof, the method comprising the steps of: a) culturing the host cell containing an expression vector containing at least a fragment of the polynucleotide sequence encoding an HRM under conditions suitable for the expression of the polypeptide; and b) recovering the polypeptide from the host cell culture.

15 The invention also provides a pharmaceutical composition comprising a substantially purified HRM in conjunction with a suitable pharmaceutical carrier.

The invention also provides a purified antagonist of HRM. In one aspect the invention provides a purified antibody which binds to an HRM.

Still further, the invention provides a purified agonist of HRM.

20 The invention also provides a method for treating or preventing a cancer comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition containing HRM.

The invention also provides a method for treating or preventing a cancer comprising administering to a subject in need of such treatment an effective amount of an antagonist of
25 HRM.

The invention also provides a method for treating or preventing an immune response associated with the increased expression or activity of HRM comprising administering to a subject in need of such treatment an effective amount of an antagonist of HRM.

The invention also provides a method for stimulating cell proliferation comprising
30 administering to a cell an effective amount of purified HRM.

The invention also provides a method for detecting a polynucleotide which encodes a human regulatory molecule in a biological sample comprising the steps of: a) hybridizing a

polynucleotide sequence complementary to a polynucleotide encoding HRM to nucleic acid material of a biological sample, thereby forming a hybridization complex; and b) detecting the hybridization complex, wherein the presence of the complex correlates with the presence of a polynucleotide encoding the human regulatory molecule in the biological sample.

5 The invention also provides a microarray which contains at least a fragment of at least one of the polynucleotide sequences encoding HRM. In a particular aspect, the microarray contains at least a fragment of at least one of the sequences selected from the group consisting of SEQ ID NOs:11-20.

10 The invention also provides a method for the simultaneous detection of the levels of expression of polynucleotides which encode human regulatory molecules in a biological sample comprising the steps of: a) hybridizing said microarray to labeled complementary nucleotides of a biological sample, comprising at least a fragment of at least one of the polynucleotides encoding HRM, thereby forming hybridization complexes; and b) quantifying expression, wherein the signal produced by the hybridization complexes
15 correlates with expression of particular polynucleotides encoding human regulatory molecules in the biological sample. In a preferred embodiment, prior to hybridization, the nucleic acid material of the biological sample is amplified and labeled by the polymerase chain reaction.

DESCRIPTION OF THE INVENTION

20 Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular methodology, protocols, cell lines, vectors, and reagents described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

25 It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a host cell" includes a plurality of such host cells, reference to the "antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

30 Unless defined otherwise, all technical and scientific terms used herein have the same meanings commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein

can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are incorporated herein by reference for the purpose of describing and disclosing the cell lines, vectors, arrays and methodologies which are reported in the publications which might be used in connection with
5 the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

HRM refers to the amino acid sequences of substantially purified HRM obtained from any species, particularly mammalian, including bovine, ovine, porcine, murine, equine,
10 and preferably human, from any source whether natural, synthetic, semi-synthetic, or recombinant.

"Agonist" refers to a molecule which, when bound to HRM, increases or prolongs the duration of the effect of HRM. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of HRM.

15 An "allele" or "allelic sequence" is an alternative form of the gene encoding HRM. Alleles may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions,
20 additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding HRM include those with deletions, insertions, or substitutions of different nucleotides resulting in a polynucleotide that encodes the same or a functionally equivalent HRM. Included within this definition are
25 polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding HRM, and improper or unexpected hybridization to alleles, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding HRM. The encoded protein may also be "altered" and contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in
30 a functionally equivalent HRM. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological or immunological activity of

HRM is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid; positively charged amino acids may include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine, glycine and alanine, asparagine and glutamine, serine and threonine, and phenylalanine and tyrosine.

"Amino acid sequence" refers to an oligopeptide, peptide, polypeptide, or protein sequence, and fragment thereof, and to naturally occurring or synthetic molecules. Fragments of HRM are preferably about 5 to about 15 amino acids in length and retain the biological activity or the immunological activity of HRM. Where "amino acid sequence" is recited herein to refer to an amino acid sequence of a naturally occurring protein molecule, amino acid sequence, and like terms, are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

"Amplification" refers to the production of additional copies of a nucleic acid sequence and is generally carried out using polymerase chain reaction (PCR) technologies well known in the art

"Antagonist" refers to a molecule which, when bound to HRM, decreases the amount or the duration of the effect of the biological or immunological activity of HRM. Antagonists may include proteins, nucleic acids, carbohydrates, or any other molecules which decrease the effect of HRM.

"Antibody" refers to intact molecules as well as fragments thereof, such as F_a , $F(ab')_2$, and F_v , which are capable of binding the epitopic determinant. Antibodies that bind HRM polypeptides can be prepared using intact polypeptides or fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal can be derived from the translation of RNA or synthesized chemically and can be conjugated to a carrier protein, if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin and thyroglobulin, keyhole limpet hemocyanin. The coupled peptide is then used to immunize the animal (e.g., a mouse, a rat, or a rabbit).

"Antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to a given region or three-dimensional structure on the

protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

“Antisense” refers to any composition containing nucleotide sequences which are complementary to a specific DNA or RNA sequence. The term “antisense strand” is used in reference to a nucleic acid strand that is complementary to the “sense” strand. Antisense molecules include peptide nucleic acids and may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and block either transcription or translation. The designation “negative” is sometimes used in reference to the antisense strand, and “positive” is sometimes used in reference to the sense strand.

“Biologically active” refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, “immunologically active” refers to the capability of the natural, recombinant, or synthetic HRM, or any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

“Complementary” or “complementarity” refer to the natural binding of polynucleotides under permissive salt and temperature conditions by base-pairing. For example, the sequence “A-G-T” binds to the complementary sequence “T-C-A”. Complementarity between two single-stranded molecules may be “partial”, in which only some of the nucleic acids bind, or it may be complete when total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands and in the design and use of PNA molecules.

A “composition comprising a given polynucleotide sequence” refers broadly to any composition containing the given polynucleotide sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding HRM (SEQ ID NOs:11-20) or fragments thereof may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., SDS) and other components

(e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

“Consensus” refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, has been extended using XL-PCR kit (Perkin Elmer, Norwalk CT) in the 5' and/or the 3' direction and resequenced, or has been assembled from the overlapping
5 sequences of more than one Incyte Clone using a computer program for fragment assembly (e.g., GELVIEW Fragment Assembly system, GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

The phrase “correlates with expression of a polynucleotide” indicates that the detection of the presence of a ribonucleic acid that is similar to a polynucleotide encoding an
10 HRM by northern analysis is indicative of the presence of mRNA encoding HRM in a sample and thereby correlates with expression of the transcript from the polynucleotide encoding the protein.

“HRM” refers to any or all of the human polypeptides. HRM-1 through HRM-10.

“Deletion” refers to a change in the amino acid or nucleotide sequence and results in
15 the absence of one or more amino acid residues or nucleotides.

“Derivative” refers to the chemical modification of a nucleic acid encoding or complementary to HRM or the encoded HRM. Such modifications include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A nucleic acid derivative encodes a polypeptide which retains the biological or immunological function of the natural molecule.
20 A derivative polypeptide is one which is modified by glycosylation, pegylation, or any similar process which retains the biological or immunological function of the polypeptide from which it was derived.

“Homology” refers to a degree of complementarity. There may be partial homology or complete homology (i.e., identity). A partially complementary sequence that at least
25 partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to using the functional term “substantially homologous.” The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or hybridization probe
30 will compete for and inhibit the binding of a completely homologous sequence to the target sequence under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require

that the binding of two sequences to one another be a specific (i.e., selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% identity). In the absence of non-specific binding, the probe will not hybridize to the second non-
5 complementary target sequence.

Human artificial chromosomes (HACs) are linear microchromosomes which may contain DNA sequences of 10K to 10M in size and contain all of the elements required for stable mitotic chromosome segregation and maintenance.

“Humanized antibody” refers to antibody molecules in which amino acids have been
10 replaced in the non-antigen binding regions in order to more closely resemble a human antibody, while still retaining the original binding ability.

“Hybridization” refers to any process by which a strand of nucleic acid bonds with a complementary strand through base pairing.

“Hybridization complex” refers to a complex formed between two nucleic acid
15 sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g., C_{0t} or R_{0t} analysis) or between one nucleic acid sequence present in solution
20 and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

An “insertion” or “addition” refers to a change in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides,
25 respectively, as compared to the naturally occurring molecule.

“Microarray” refers to an array (or arrangement) of distinct oligonucleotides synthesized on a substrate, such as paper, nylon or other type of membrane, filter, gel, polymer, chip, glass slide, or any other suitable support.

“Modulate” refers to a change in the activity of HRM. For example, modulation may
30 cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional or immunological properties of HRM.

“Nucleic acid sequence” refers to an oligonucleotide, nucleotide, or polynucleotide,

and fragments thereof, and to DNA or RNA of genomic or synthetic origin which may be single- or double-stranded, and represent the sense or antisense strand. "Fragments" are those nucleic acid sequences which are greater than 60 nucleotides in length, and most preferably includes fragments that are at least 100 nucleotides or at least 1000 nucleotides, and at least 10,000 nucleotides in length.

"Oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20 to 25 nucleotides, which can be used in PCR amplification or hybridization assays. As used herein, oligonucleotide is substantially equivalent to the terms "amplimers", "primers", "oligomers", and "probes", as commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least five nucleotides in length linked to a peptide backbone of amino acid residues which ends in lysine. The terminal lysine confers solubility to the composition. PNAs may be pegylated to extend their lifespan in the cell where they preferentially bind complementary single stranded DNA and RNA and stop transcript elongation (Nielsen, P.E. et al. (1993) Anticancer Drug Des. 8:53-63).

"Portion", with regard to a protein (as in "a portion of a given protein"), refers to fragments of that protein. The fragments may range in size from five amino acid residues to the entire amino acid sequence minus one amino acid. Thus, a protein "comprising at least a portion of the amino acid sequence of an HRM encompasses the full-length HRM and fragments thereof.

"Sample" is used in its broadest sense. A biological sample suspected of containing nucleic acid encoding HRM, or fragments thereof, or HRM itself may comprise a bodily fluid, extract from a cell, chromosome, organelle, or membrane isolated from a cell, a cell, genomic DNA, RNA, or cDNA (in solution or bound to a solid support, a tissue, a tissue print, and the like.

"Specific binding" or "specifically binding" refers to that interaction between a protein or peptide and an agonist, an antibody and an antagonist. The interaction is dependent upon the presence of a particular structure (i.e., the antigenic determinant or epitope) of the protein recognized by the binding molecule. For example, if an antibody is specific for epitope "A", the presence of a protein containing epitope A (or free, unlabeled A) in a reaction containing labeled "A" and the antibody will reduce the amount of labeled A bound

to the antibody.

"Stringent conditions" or "stringency" refer to the conditions for hybridization as defined by the nucleic acid, salt, and temperature. These conditions are well known in the art and may be altered in order to identify or detect identical or related polynucleotide sequences.

- 5 Numerous equivalent conditions comprising either low or high stringency depend on factors such as the length and nature of the sequence (DNA, RNA, base composition), nature of the target (DNA, RNA, base composition), milieu (in solution or immobilized on a solid substrate), concentration of salts and other components (e.g., formamide, dextran sulfate and/or polyethylene glycol), and temperature of the reactions (within a range from about 5°C
- 10 below the melting temperature of the probe to about 20°C to 25°C below the melting temperature). One or more factors may be varied to generate conditions of either low or high stringency different from, but equivalent to, the above listed conditions.

- "Substantially purified" refers to nucleic or amino acid sequences that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably
- 15 75% free, and most preferably 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

- "Transformation" describes a process by which exogenous DNA enters and changes a
- 20 recipient cell. It may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. Such
- 25 "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time.

- A "variant" of HRM refers to an amino acid sequence that is altered by one or more
- 30 amino acids. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More rarely, a variant may have "nonconservative" changes, e.g., replacement of a glycine

with a tryptophan. Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software

5 (DNASTAR Inc., Madison WI)

THE INVENTION

The invention is based on the discovery of human regulatory molecules (HRM) and the polynucleotides encoding HRM and on the use of these compositions for the diagnosis, prevention, or treatment of diseases associated with cell proliferation. Table 1 shows the
10 protein and nucleotide sequence identification numbers, protein abbreviation, Incyte Clone number, cDNA library, NCBI homolog and NCBI sequence identifier for each of the human regulatory molecules disclosed herein.

5 HRM-1 (SEQ ID NO:1) was identified in Incyte Clone 9476 from the HMC1NOT01 cDNA library using a computer search for amino acid sequence alignments. A consensus
15 sequence, SEQ ID NO:11, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 9476 (HMC1NOT01), 010403 (THP1PLB01), 495099 (HNT2NOT01), 1670783 (BMARNOT03), 1997203 (BRSTTUT03), and 2190637 (THYRTUT03).

In one embodiment, the invention encompasses a polypeptide comprising the amino
20 acid sequence of SEQ ID NO:1. HRM-1 is 456 amino acids in length and has a potential N glycosylation site at N385; 14 potential phosphorylation sites at T9, T12, S58, T74, T163, T139, S175, T211, T239, T272, S331, T367, T402, and S443; and an ATP/GTP binding motif at G₇₀PPGTGKT77. HRM-1 has sequence homology with a *S. cerevisiae* protein (g755784) and is found in cDNA libraries which have dividing, cancerous or immortalized
25 cells and are associated with immune response.

8 HRM-2 (SEQ ID NO:2) was identified in Incyte Clone 77180 from the SYNORAB01 cDNA library using a computer search for amino acid sequence alignments. A consensus
sequence, SEQ ID NO:12, was derived from the extended and overlapping nucleic acid
sequences: Incyte Clones 077180 (SYNORAB01), 604706 (BRSTTUT01), 977901
30 (BRSTNOT02), 1870373 (SKINBIT01), and 2169441 (ENDCNOT03).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:2. HRM-2 is 188 amino acids in length and has one potential

amidation site, Q170GKR; two potential N glycosylation sites at N60 and N68; and four potential phosphorylation sites at S70, T164, T166, and S183. HRM-2 has sequence homology with a S. cerevisiae protein (g5372) and is found in cDNA libraries which have dividing, cancerous or immortalized cells and are associated with immune response.

3 HRM-3 (SEQ ID NO:3) was identified in Incyte Clone 118160 from the MUSCNOT01 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:13, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 118160 (MUSCNOT01), 323015 (EOSIHET02), and 1856519 (PROSNOT18).

10 In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:3. HRM-3 is 348 amino acids in length and has two potential N glycosylation sites at N150 and N317; 17 potential phosphorylation sites at T23, T45, S60, T126, S130, S140, S145, S151, S154, S158, S186, Y208, Y234, S217, T271, T303, and S327, and a transcription factor signature at C₃₁₀SKCKKKNCTYNQVQTRSA

15 DEPMTTTFVLCNEC. HRM-3 has sequence homology with a Mus musculus protein (g220594) and is found in cDNA libraries which have secretory or immune associations.

21 HRM-4 (SEQ ID NO:4) was identified in Incyte Clone 933353 from the CERVNOT01 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:14, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 928904 (BRAINOT04), 933353 (CERVNOT01), and 2452674 (ENDANOT01).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:4. HRM-4 is 201 amino acids in length and has one potential N glycosylation site at N82; five potential phosphorylation sites at T70, S83, S98, S154, and T187; and one tyrosine phosphatase motif at V₁₃₀HCKAGRSRSATM. HRM-4 has sequence homology with a C. elegans protein (g1657672) and is found in cDNA libraries associated with immune response.

24 HRM-5 (SEQ ID NO:5) was identified in Incyte Clone 1404643 from the LATRTUT02 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:15, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 878243 (LUNGAST01), 1404643 (LATRTUT02), 1508343 (LUNGNOT14) and 2585156 (BRAITUT22).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:5. HRM-5 is 239 amino acids in length and has four potential phosphorylation sites at S5, S89, S133, and T211. HRM-5 has sequence homology with a *C. elegans* protein (g459002) and is found in cDNA libraries associated with cell proliferation, cancer and immune response.

30 HRM-6 (SEQ ID NO:6) was identified in Incyte Clone 1600438 from the BLADNOT03 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:16, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 835283 (PROSNOT07), 1600044 (BLADNOT03), 1600438
10 (BLADNOT03), and 1922072 (BRSTTUT01).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:6. HRM-6 is 419 amino acids in length and has one potential N glycosylation site at N161; twelve potential phosphorylation sites at T16, S57, T67, T83, S100, T107, S144, S206, T254, Y351, S412, and S414; a leucine zipper motif,
15 L₃₈NEAGDDLEAVAKFLDSTGSRL; and an ATP/GTP binding motif, A₃₈₅HVAKGKS. HRM-6 has sequence homology with human KIAA0005 (g286001) and is found in cDNA libraries associated with secretion and cancer.

33 HRM-7 (SEQ ID NO:7) was identified in Incyte Clone 1600518 from the BLADNOT03 cDNA library using a computer search for amino acid sequence alignments. A
20 consensus sequence, SEQ ID NO:17, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 389679 (THYMNOT02), 1600518 (BLADNOT03), 2055734 (BEPINOT01), 2102793 (BRAITUT02), and 2509270 (CONUTUT01).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:7. HRM-7 is 376 amino acids in length and has one potential N
25 glycosylation site at N161 and 14 potential phosphorylation sites at T30, S65, S75, S95, S106, T134, S159, S224, T228, T250, T292, S299, T303, and S323 and a glycosaminoglycan motif, S14GPG. HRM-7 has sequence homology with a *C. elegans* protein (g790405) and is found in cDNA libraries associated with immune response, secretion, and cancer.

45 HRM-8 (SEQ ID NO:8) was identified in Incyte Clone 2515476 from the LIVRTUT04 cDNA library using a computer search for amino acid sequence alignments. A
30 consensus sequence, SEQ ID NO:18, was derived from the extended and overlapping nucleic acid sequences: Incyte clones 18414 (HUVELPB01), 78341 (SYNORAB01), 143277

(TLYMNOR01), 181574 (PLACNOB01), 832996 (PROSTUT04), 962753 (BRSTTUT03), 1413604 (BRAINOT12), and 2515476 (LIVRTUT04).

In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:8. HRM-8 is 811 amino acids in length and has three potential
 5 amidation sites at G₁₁₃GRR, W₁₆₅GKR, and G₇₉₀GKK; four potential N glycosylation sites at N22, N56, N79, and N145; 24 potential phosphorylation sites at T11, S13, S30, S60, Y71, S81, S85, S86, S103, S254, S256, T377, S388, S425, S456, S487, T544, S552, S574, T659, S678, S702, S746, and S753; a potential glycosaminoglycan site, S₁₆₀GHG; and a potential
 10 zinc finger motif at C₂₄₀GHIFCWACI. HRM-8 has sequence homology with human KIAA0262 (g1665790) and is found in cDNA libraries involved in cell proliferation, secretion, cancer, and immune response.

46 HRM-9 (SEQ ID NO:9) was identified in Incyte Clone 2754573 from the THP1AZS08 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:19, was derived from the extended and overlapping nucleic
 15 acid sequences: Incyte Clones 263630 (HNT2AGT01), 412307 (BRSTNOT01), 491644 (HNT2AGT01), 1253094 (LUNGFET03), 2270603 (PROSNON01), 2280508 (PROSNON01), 2375670 (ISLTNOT01), 2754573 (THP1AZS08), and 3151587 (ADRENON04).

In one embodiment, the invention encompasses a polypeptide comprising the amino
 20 acid sequence of SEQ ID NO:9. HRM-9 is 352 amino acids in length and has two potential N glycosylation sites at N141 and N294, and thirteen potential phosphorylation sites at S8, T67, T106, T110, T121, S122, S169, S206, T210, S215, S256, S260, and T296. HRM-9 has sequence homology with human RNA binding protein (g478990) and is found in cDNA libraries involved in cell proliferation, secretion, and immune response.

25 47 HRM-10 (SEQ ID NO:10) was identified in Incyte Clone 2926777 from the TLYMNOT04 cDNA library using a computer search for amino acid sequence alignments. A consensus sequence, SEQ ID NO:20, was derived from the extended and overlapping nucleic acid sequences: Incyte Clones 040208 (TBLYNOT01), 900242 (BRSTTUT03), 963500 (BRSTTUT03), 1996474 (BRSTTUT03), and 2926777 (TLYMNOT04).

30 In one embodiment, the invention encompasses a polypeptide comprising the amino acid sequence of SEQ ID NO:10. HRM-10 is 432 amino acids in length and has a potential N glycosylation site at N417 and 24 potential phosphorylation sites at T51, S73, T122, T133,

S177, S206, T226, T238, S293, S300, S304, S309, T325, S333, S339, S353, S360, Y361, S384, S390, T403, T412, T419, and S425. HRM-10 has sequence homology with a C. elegans protein (g687823) and is found in cDNA libraries involved in cell proliferation, secretion, cancer, and immune response.

5 The invention also encompasses HRM variants which retain the biological or functional activity of HRM. A preferred HRM variant is one having at least 80%, and more preferably 90%, amino acid sequence identity to the HRM amino acid sequence. A most preferred HRM variant is one having at least 95% amino acid sequence identity to an HRM disclosed herein (SEQ ID NOs: 1-10).

10 The invention also encompasses polynucleotides which encode HRM. Accordingly, any nucleic acid sequence which encodes the amino acid sequence of HRM can be used to produce recombinant molecules which express HRM. In a particular embodiment, the invention encompasses a polynucleotide consisting of a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 11-20.

15 It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding HRM, some bearing minimal homology to the nucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of nucleotide sequence that could be made by selecting combinations based on possible codon choices.

20 These combinations are made in accordance with the standard triplet genetic code as applied to the nucleotide sequence of naturally occurring HRM, and all such variations are to be considered as being specifically disclosed.

 Although nucleotide sequences which encode HRM and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring HRM under
25 appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding HRM or its derivatives possessing a substantially different codon usage. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the
30 nucleotide sequence encoding HRM and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences, or fragments thereof, which encode HRM and its derivatives, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents that are well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding HRM or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed nucleotide sequences, and in particular, those shown in SEQ ID NOs:11-20, under various conditions of stringency as taught in Wahl, G.M. and S.L. Berger (1987; Methods Enzymol. 152:399-407) and Kimmel, A.R. (1987; Methods Enzymol. 152:507-511).

Methods for DNA sequencing which are well known and generally available in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical Corp, Cleveland OH), TAQ polymerase (Perkin Elmer), thermostable T7 polymerase (Amersham Pharmacia, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system marketed by Life Technologies (Gaithersburg MD). Preferably, the process is automated with machines such as the Hamilton Micro Lab 2200 (Hamilton, Reno NV), Peltier Thermal Cycler (PTC200; MJ Research, Watertown MA) and the ABI Catalyst and 373 and 377 DNA Sequencers (Perkin Elmer).

The nucleic acid sequences encoding HRM may be extended utilizing a partial nucleotide sequence and employing various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, one method which may be employed, "restriction-site" PCR, uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, G. (1993) PCR Methods Applic. 2:318-322). In particular, genomic DNA is first amplified in the presence of primer to a linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR may also be used to amplify or extend sequences using divergent primers based on a known region (Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186). The primers

may be designed using commercially available software such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth MN), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. The method uses several restriction enzymes to
5 generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which may be used is capture PCR which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119). In this
10 method, multiple restriction enzyme digestions and ligations may also be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR.

Another method which may be used to retrieve unknown sequences is that of Parker, J.D. et al. (1991: Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested
15 primers, and PROMOTERFINDER libraries to walk genomic DNA (Clontech, Palo Alto CA). This process avoids the need to screen libraries and is useful in finding intron/exon junctions. When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Also, random-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a
20 randomly primed library may be especially preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In
25 particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin Elmer) and the entire process from loading of
30 samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA which might be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode HRM may be used in recombinant DNA molecules to direct expression of HRM, fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced, and these sequences may be used to clone and express HRM.

As will be understood by those of skill in the art, it may be advantageous to produce HRM-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter HRM encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding HRM may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of HRM activity, it may be useful to encode a chimeric HRM protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the HRM encoding sequence and the heterologous protein sequence, so that HRM may be cleaved and purified away from the heterologous moiety.

In another embodiment, sequences encoding HRM may be synthesized, in whole or in part, using chemical methods well known in the art. (See Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223; Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.) Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of HRM, or a fragment thereof. For example, peptide synthesis can be

performed using various solid-phase techniques (Roberge, J.Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide synthesizer (Perkin Elmer).

The newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) Proteins, Structures and Molecular Principles, WH Freeman and Co., New York NY). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; Creighton, supra). Additionally, the amino acid sequence of HRM, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a biologically active HRM, the nucleotide sequences encoding HRM or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence.

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding HRM and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. Such techniques are described in Sambrook, J. et al. (1989; Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY) and Ausubel, F.M. et al. (1989; Current Protocols in Molecular Biology, John Wiley & Sons, New York NY).

A variety of expression vector/host systems may be utilized to contain and express sequences encoding HRM. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

The "control elements" or "regulatory sequences" are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host

cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible
5 promoters such as the hybrid lacZ promoter of the BLUESCRIPT phagemid (Stratagene, LaJolla CA) or pSPORT1 plasmid (Life Technologies) and the like may be used. The baculovirus polyhedrin promoter may be used in insect cells. Promoters or enhancers derived from the genomes of plant cells (e.g., heat shock, RUBISCO; and storage protein genes) or from plant viruses (e.g., viral promoters or leader sequences) may be cloned into the vector.
10 In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding HRM, vectors based on SV40 or EBV may be used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon
15 the use intended for HRM. For example, when large quantities of HRM are needed for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding HRM may be ligated into the vector in frame with sequences for the
20 amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509); and the like. pGEX vectors (Promega, Madison WI) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by
25 adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or
30 inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987: Methods Enzymol. 153:516-544).

In cases where plant expression vectors are used, the expression of sequences

encoding HRM may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (McGraw Hill Yearbook of Science and Technology 10 (1992) McGraw Hill, New York NY; pp. 191-196).

An insect system may also be used to express HRM. For example, in one such system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in Spodoptera frugiperda cells or in Trichoplusia larvae. The sequences encoding HRM may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of HRM will 15 render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, S. frugiperda cells or Trichoplusia larvae in which HRM may be expressed (Engelhard, E.K. et al. (1994) Proc. Nat. Acad. Sci. 91:3224-3227).

20 In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding HRM may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing HRM in infected 25 host cells (Logan, J. and Shenk, T. (1984) Proc. Natl. Acad. Sci. 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained and expressed in a plasmid. HACs of 6 to 10M are 30 constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes (Harrington, J.J. et al. (1997) Nat Genet. 15:345-355).

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding HRM. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding HRM, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; Bethesda MD) and may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express HRM may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines.

These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. et al. (1977) Cell 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1980) Cell 22:817-23) genes which can be employed in tk⁻ or apt⁻ cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-70); npt, which confers resistance to the aminoglycosides neomycin and G-418 (Colbere-Garapin, F. et al (1981) J. Mol. Biol. 150:1-14) and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (McGraw Hill Yearbook of Science and Technology, supra). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of histidine (Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-51). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, β glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C.A. et al. (1995) Methods Mol. Biol. 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding HRM is inserted within a marker gene sequence, transformed cells containing sequences encoding HRM can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding HRM under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain the nucleic acid sequence encoding HRM and express HRM may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

The presence of polynucleotide sequences encoding HRM can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments or fragments of polynucleotides encoding HRM. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on the sequences encoding HRM to

detect transformants containing DNA or RNA encoding HRM.

A variety of protocols for detecting and measuring the expression of HRM, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA),
5 and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on HRM is preferred, but a competitive binding assay may be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul MN) and Maddox, D.E. et al. (1983; J. Exp. Med. 158:1211-1216).

10 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding HRM include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding HRM, or any fragments
15 thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits (Amersham Pharmacia, Promega; and US Biochemical Corp.). Suitable reporter
20 molecules or labels, which may be used for ease of detection, include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding HRM may be cultured under conditions suitable for the expression and recovery of the protein from cell culture.
25 The protein produced by a transformed cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode HRM may be designed to contain signal sequences which direct secretion of HRM through a prokaryotic or eukaryotic cell membrane. Other constructions may be used to join sequences encoding
30 HRM to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on

immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle WA). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego CA) between the purification domain and HRM may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing HRM and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMAC (immobilized metal ion affinity chromatography as described in Porath, J. et al. (1992, Prot. Exp. Purif. 3: 263-281) while the enterokinase cleavage site provides a means for purifying HRM from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D.J. et al. (1993; DNA Cell Biol. 12:441-453).

In addition to recombinant production, fragments of HRM may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) J. Am. Chem. Soc. 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide synthesizer (Perkin Elmer). Various fragments of HRM may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

20 THERAPEUTICS

Chemical and structural homology exists among the human regulatory proteins of the invention. The expression of HRM is closely associated with cell proliferation. Therefore, in cancers or immune disorders where HRM is an activator, transcription factor, or enhancer, and is promoting cell proliferation; it is desirable to decrease the expression of HRM. In cancers where HRM is an inhibitor or suppressor and is controlling or decreasing cell proliferation, it is desirable to provide the protein or to increase the expression of HRM.

In one embodiment, where HRM is an inhibitor, HRM or a fragment or derivative thereof may be administered to a subject to prevent or treat a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, and teratocarcinoma. Such cancers include, but are not limited to, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis,

thymus, thyroid, and uterus.

In another embodiment, an agonist which is specific for HRM may be administered to a subject to prevent or treat a cancer including, but not limited to, those cancers listed above.

In another further embodiment, a vector capable of expressing HRM, or a fragment or a derivative thereof, may be administered to a subject to prevent or treat a cancer including, but not limited to, those cancers listed above.

In a further embodiment where HRM is promoting cell proliferation, antagonists which decrease the expression or activity of HRM may be administered to a subject to prevent or treat a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, and teratocarcinoma. Such cancers include, but are not limited to, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. In one aspect, antibodies which specifically bind HRM may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express HRM.

In another embodiment, a vector expressing the complement of the polynucleotide encoding HRM may be administered to a subject to treat or prevent a cancer including, but not limited to, those cancers listed above.

In yet another embodiment where HRM is promoting leukocyte activity or proliferation, antagonists which decrease the activity of HRM may be administered to a subject to prevent or treat an immune response. Such responses may be associated with AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, gout, Graves' disease, hypereosinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjögren's syndrome, and autoimmune thyroiditis; complications of cancer, hemodialysis, extracorporeal circulation; viral, bacterial, fungal, parasitic, protozoal, and helminthic infections; and trauma. In one aspect, antibodies which specifically bind HRM may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical

agent to cells or tissue which express HRM.

In another embodiment, a vector expressing the complement of the polynucleotide encoding HRM may be administered to a subject to treat or prevent an immune response including, but not limited to, those listed above

5 In one further embodiment, HRM or a fragment or derivative thereof may be added to cells to stimulate cell proliferation. In particular, HRM may be added to a cell in culture or cells in vivo using delivery mechanisms such as liposomes, viral based vectors, or electroinjection for the purpose of promoting cell proliferation and tissue or organ regeneration. Specifically, HRM may be added to a cell, cell line, tissue or organ culture in
10 vitro or ex vivo to stimulate cell proliferation for use in heterologous or autologous transplantation. In some cases, the cell will have been preselected for its ability to fight an infection or a cancer or to correct a genetic defect in a disease such as sickle cell anemia, β thalassemia, cystic fibrosis, or Huntington's chorea.

In another embodiment, an agonist which is specific for HRM may be administered to
15 a cell to stimulate cell proliferation, as described above.

In another embodiment, a vector capable of expressing HRM, or a fragment or a derivative thereof, may be administered to a cell to stimulate cell proliferation, as described above.

In other embodiments, any of the therapeutic proteins, antagonists, antibodies, agonists, complementary sequences or vectors of the invention may be administered in
20 combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above.
25 Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

Antagonists or inhibitors of HRM may be produced using methods which are generally known in the art. In particular, purified HRM may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind HRM.

30 Antibodies to HRM may be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and fragments produced by a Fab expression library. Neutralizing

antibodies, (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others, may be immunized by injection with HRM or any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to HRM have an amino acid sequence consisting of at least five amino acids and more preferably at least 10 amino acids. It is also preferable that they are identical to a portion of the amino acid sequence of the natural protein, and they may contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of HRM amino acids may be fused with those of another protein such as keyhole limpet hemocyanin and antibody produced against the chimeric molecule.

Monoclonal antibodies to HRM may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120).

In addition, techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can be used (Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce HRM-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries (Burton D.R. (1991) Proc. Natl. Acad. Sci.

88:11120-3).

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. 86:

5 3833-3837; Winter, G. et al. (1991) Nature 349:293-299).

Antibody fragments which contain specific binding sites for HRM may also be generated. For example, such fragments include, but are not limited to, the F(ab')₂ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments.

10 Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse, W.D. et al. (1989) Science 254:1275-1281).

Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric
15 assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between HRM and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering HRM epitopes is preferred, but a competitive binding assay may also be employed (Maddox, supra).

20 In another embodiment of the invention, the polynucleotides encoding HRM, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding HRM may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding HRM. Thus,
25 complementary molecules or fragments may be used to modulate HRM activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments, can be designed from various locations along the coding or control regions of sequences encoding HRM.

Expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses,
30 or from various bacterial plasmids may be used for delivery of nucleotide sequences to the targeted organ, tissue or cell population. Methods which are well known to those skilled in the art can be used to construct vectors which will express nucleic acid sequence which is

complementary to the polynucleotides of the gene encoding HRM. These techniques are described both in Sambrook et al. (supra) and in Ausubel et al. (supra).

5 Genes encoding HRM can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide or fragment thereof which encodes HRM. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector and even longer if appropriate replication elements are part of the vector system.

10 As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5' or regulatory regions of the gene encoding HRM (signal sequence, promoters, enhancers, and introns). Oligonucleotides derived from the transcription initiation site, e.g., between positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature (Gee, J.E. et al. (1994) In: Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, NY). The complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

20 Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples which may be used include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding HRM.

30 Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for secondary structural features which may render the

oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding HRM. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA constitutively or inducibly can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections or polycationic amino polymers (Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-66; incorporated herein by reference) may be achieved using methods which are well known in the art.

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of HRM, antibodies to HRM, mimetics, agonists, antagonists, or inhibitors of HRM.

The compositions may be administered alone or in combination with at least one other agent, such as stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel,

polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of HRM, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models, usually mice, rabbits, dogs, or pigs. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example HRM or fragments thereof, antibodies of HRM, agonists, antagonists or inhibitors of HRM, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ' (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index, and it can be expressed as the ratio, ED50/LD50.

Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or once

every two weeks depending on half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind HRM may be used for the diagnosis of conditions or diseases characterized by expression of HRM, or in assays to monitor patients being treated with HRM, agonists, antagonists or inhibitors. The antibodies useful for diagnostic purposes may be prepared in the same manner as those described above for therapeutics. Diagnostic assays for HRM include methods which utilize the antibody and a label to detect HRM in human body fluids or extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. A wide variety of reporter molecules which are known in the art may be used, several of which are described above.

A variety of protocols including ELISA, RIA, and FACS for measuring HRM are known in the art and provide a basis for diagnosing altered or abnormal levels of HRM expression. Normal or standard values for HRM expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to HRM under conditions suitable for complex formation. The amount of standard complex formation may be quantified by various methods, but preferably by photometric means. Quantities of HRM expressed in subject, control and disease, samples are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding HRM may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of HRM may be correlated with disease. The diagnostic assay may be used to distinguish between absence, presence, and excess expression of HRM, and to monitor

regulation of HRM levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding HRM or closely related molecules, may be used to identify nucleic acid sequences which encode HRM. The
5 specificity of the probe, whether it is made from a highly specific region, e.g., 10 unique nucleotides in the 5' regulatory region, or a less specific region, e.g., especially in the 3' coding region, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low) will determine whether the probe identifies only naturally occurring sequences encoding HRM, alleles, or related sequences.

10 Probes may also be used for the detection of related sequences, and should preferably contain at least 50% of the nucleotides from any of the HRM encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and derived from the nucleotide sequence of SEQ ID Nos: 11-20 or from genomic sequence including promoter, enhancer elements, and introns of the naturally occurring HRM.

15 Means for producing specific hybridization probes for DNAs encoding HRM include the cloning of nucleic acid sequences encoding HRM or HRM derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be
20 labeled by a variety of reporter groups, for example, radionuclides such as ³²P or ³⁵S, or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding HRM may be used for the diagnosis of conditions, disorders, or diseases which are associated with either increased or decreased expression of
25 HRM. Examples of such conditions or diseases include adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and cancers of the adrenal gland, bladder, bone, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, bone marrow, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and immune disorders such as AIDS,
30 Addison's disease, adult respiratory distress syndrome, allergies, anemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, atrophic gastritis, glomerulonephritis, gout,

Graves' disease, hypereosinophilia, irritable bowel syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, rheumatoid arthritis, scleroderma, Sjögren's syndrome, and thyroiditis. The polynucleotide sequences encoding HRM may be used in

5 Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; or in dipstick, pin, ELISA-like assays or microarrays utilizing fluids or tissues from patient biopsies to detect altered HRM expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding HRM may be useful in

10 assays that detect activation or induction of various cancers, particularly those mentioned above. The nucleotide sequences encoding HRM may be labeled by standard methods, and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the

15 biopsied or extracted sample is significantly altered from that of a comparable control sample, the nucleotide sequences have hybridized with nucleotide sequences in the sample, and the presence of altered levels of nucleotide sequences encoding HRM in the sample indicates the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or in monitoring

20 the treatment of an individual patient.

In order to provide a basis for the diagnosis of disease associated with expression of HRM, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, which encodes HRM, under conditions suitable for

25 hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with those from an experiment where a known amount of a substantially purified polynucleotide is used. Standard values obtained from normal samples may be compared with values obtained from samples from patients who are symptomatic for disease. Deviation between standard and subject values is used to establish

30 the presence of disease.

Once disease is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to evaluate whether the level of expression in the patient

begins to approximate that which is observed in the normal patient. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of a relatively high amount of transcript in
5 biopsied tissue from an individual may indicate a predisposition for the development of the disease or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

10 Additional diagnostic uses for oligonucleotides designed from the sequences encoding HRM may involve the use of PCR. Such oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably consist of two nucleotide sequences, one with sense orientation (5'→3') and another with antisense (3'←5'), employed under optimized conditions for identification of a specific gene or condition. The
15 same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of HRM include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and
20 standard curves onto which the experimental results are interpolated (Melby, P.C. et al. (1993) J. Immunol. Methods, 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 229-236). The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA-like format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

25 In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously (to produce a transcript image), and to identify genetic variants, mutations and polymorphisms. This information may be used to determine gene function, understanding the
30 genetic basis of disease, diagnosing disease, and in developing and in monitoring the activities of therapeutic agents.

In one embodiment, the microarray is prepared and used according to the methods

described in PCT application WO95/11995 (Chee et al.), Lockhart, D. J. et al. (1996; Nat. Biotech. 14: 1675-1680) and Schena, M. et al. (1996; Proc. Natl. Acad. Sci. 93: 10614-10619), all of which are incorporated herein in their entirety by reference.

The microarray is preferably composed of a large number of unique, single-stranded
5 nucleic acid sequences, usually either synthetic antisense oligonucleotides or fragments of
cDNAs, fixed to a solid support. The oligonucleotides are preferably about 6-60 nucleotides
in length, more preferably 15-30 nucleotides in length, and most preferably about 20-25
nucleotides in length. For a certain type of microarray, it may be preferable to use
oligonucleotides which are only 7-10 nucleotides in length. The microarray may contain
10 oligonucleotides which cover the known 5', or 3', sequence, or contain sequential
oligonucleotides which cover the full length sequence; or unique oligonucleotides selected
from particular areas along the length of the sequence. Polynucleotides used in the
microarray may be oligonucleotides that are specific to a gene or genes of interest in which at
least a fragment of the sequence is known or that are specific to one or more unidentified
15 cDNAs which are common to a particular cell or tissue type or to a normal, developmental, or
disease state. In certain situations it may be appropriate to use pairs of oligonucleotides on a
microarray. The "pairs" will be identical, except for one nucleotide which preferably is
located in the center of the sequence. The second oligonucleotide in the pair (mismatched by
one) serves as a control. The number of oligonucleotide pairs may range from 2 to one
20 million.

In order to produce oligonucleotides to a known sequence for a microarray, the gene
of interest is examined using a computer algorithm which starts at the 5' or more preferably at
the 3' end of the nucleotide sequence. The algorithm identifies oligomers of defined length
that are unique to the gene, have a GC content within a range suitable for hybridization, and
25 lack predicted secondary structure that may interfere with hybridization. In one aspect, the
oligomers are synthesized at designated areas on a substrate using a light-directed chemical
process. The substrate may be paper, nylon or other type of membrane, filter, chip, glass
slide, or any other suitable solid support.

In another aspect, the oligonucleotides may be synthesized on the surface of the
30 substrate by using a chemical coupling procedure and an ink jet application apparatus, as
described in PCT application WO95/251116 (Baldeschweiler et al.) which is incorporated
herein in its entirety by reference. In another aspect, a "gridded" array analogous to a dot or

slot blot (HYBRIDOT apparatus, Life Technologies) may be used to arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a vacuum system, thermal, UV, mechanical or chemical bonding procedures. In yet another aspect, an array may be produced by hand or using available devices, materials, and machines (including Brinkmann
5 multichannel pipettors or robotic instruments) and may contain 8, 24, 96, 384, 1536 or 6144 oligonucleotides, or any other multiple from 2 to one million which lends itself to the efficient use of commercially available instrumentation.

In order to conduct sample analysis using the microarrays, polynucleotides are extracted from a biological sample. The biological samples may be obtained from any bodily
10 fluid (blood, urine, saliva, phlegm, gastric juices, etc.), cultured cells, biopsies, or other tissue preparations. To produce probes, the polynucleotides extracted from the sample are used to produce nucleic acid sequences which are complementary to the nucleic acids on the microarray. If the microarray consists of cDNAs, antisense RNAs (aRNA) are appropriate probes. Therefore, in one aspect, mRNA is used to produce cDNA which, in turn and in the
15 presence of fluorescent nucleotides, is used to produce fragment or oligonucleotide aRNA probes. These fluorescently labeled probes are incubated with the microarray so that the probe sequences hybridize to the cDNA oligonucleotides of the microarray. In another aspect, complementary nucleic acid sequences are used as probes and can also include polynucleotides, fragments, complementary, or antisense sequences produced using
20 restriction enzymes, PCR technologies, and Oligolabelling or TransProbe kits (Amersham Pharmacia) well known in the area of hybridization technology.

Incubation conditions are adjusted so that hybridization occurs with precise complementary matches or with various degrees of less complementarity. After removal of nonhybridized probes, a scanner is used to determine the levels and patterns of fluorescence.
25 The scanned images are examined to determine degree of complementarity and the relative abundance of each oligonucleotide sequence on the microarray. A detection system may be used to measure the absence, presence, and amount of hybridization for all of the distinct sequences simultaneously. This data may be used for large scale correlation studies or functional analysis of the sequences, mutations, variants, or polymorphisms among samples
30 (Heller, R.A. et al., (1997) Proc. Natl. Acad. Sci. 94:2150-55).

In another embodiment of the invention, the nucleic acid sequences which encode HRM may also be used to generate hybridization probes which are useful for mapping the

naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome or to artificial chromosome constructions, such as human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions or single chromosome cDNA libraries as reviewed in Price, C.M. (1993; Blood Rev. 7:127-134) and Trask, B.J. (1991; Trends Genet. 7:149-154).

Fluorescent in situ hybridization (FISH as described in Verma et al. (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY) may be correlated with other physical chromosome mapping techniques and genetic map data. Examples of genetic map data can be found in various scientific journals or at Online Mendelian Inheritance in Man (OMIM). Correlation between the location of the gene encoding HRM on a physical chromosomal map and a specific disease, or predisposition to a specific disease, may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier, or affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, for example, AT to 11q22-23 (Gatti, R.A. et al. (1988) Nature 336:577-580), any sequences mapping to that area may represent associated or regulatory genes for further investigation. The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc. among normal, carrier, or affected individuals.

In another embodiment of the invention, HRM, its catalytic or immunogenic fragments or oligopeptides thereof, can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The

formation of binding complexes, between HRM and the agent being tested, may be measured.

Another technique for drug screening which may be used provides for high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO84/03564. In this method, large numbers of different small
5 test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with HRM, or fragments thereof, and washed. Bound HRM is then detected by methods well known in the art. Purified HRM can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize
10 it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding HRM specifically compete with a test compound for binding HRM. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with HRM.

15 In additional embodiments, the nucleotide sequences which encode HRM may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

The examples below are provided to illustrate the subject invention and are not
20 included for the purpose of limiting the invention.

EXAMPLES

For purposes of example, the preparation and sequencing of the LNODNOT03 cDNA library, from which Incyte Clones were isolated, is described. Preparation and sequencing of cDNAs in libraries in the LIFESEQ database (Incyte Pharmaceuticals, Palo Alto CA) have
25 varied over time, and the gradual changes involved use of kits, plasmids, and machinery available at the particular time the library was made and analyzed.

I LNODNOT03 cDNA Library Construction

The LNODNOT03 cDNA library was constructed from microscopically normal lymph node tissue excised from a 67-year-old Caucasian male with lung cancer during a
30 segmental lung resection. This nontumorous tissue was associated with an invasive grade 3 squamous cell carcinoma of the lung. The patient history included hemangioma and tobacco use. The patient was taking DOXYCYCLINE, a tetracycline, to treat an infection.

The frozen tissue was homogenized and lysed using a Brinkmann Homogenizer Polytron PT-3000 (Brinkmann Instruments, Westbury NJ) in guanidinium isothiocyanate solution. The lysate was centrifuged over a 5.7 M CsCl cushion using a Beckman SW28 rotor in a Beckman L8-70M Ultracentrifuge (Beckman Coulter Instruments, Fullerton CA) for 18 hours at 25,000 rpm at ambient temperature. The RNA was extracted with acid phenol pH 4.7, precipitated using 0.3 M sodium acetate and 2.5 volumes of ethanol, resuspended in RNase-free water, and treated with DNase at 37°C. Extraction and precipitation were repeated as before. The mRNA was isolated with the OLIGOTEX kit (QIAGEN, Inc., Chatsworth CA) and used to construct the cDNA library.

The mRNA was handled according to the recommended protocols in the SUPERScript Plasmid System for cDNA synthesis and plasmid cloning (Life Technologies). The cDNAs were fractionated on a SEPHAROSE CL4B column (Amersham Pharmacia), and those cDNAs exceeding 400 bp were ligated into pINCY 1. The plasmid pINCY (Incyte Pharmaceuticals) was subsequently transformed into DH5 α competent cells (Life Technologies).

II Isolation and Sequencing of cDNA Clones

Plasmid DNA was released from the cells and purified using the REAL Prep 96 plasmid kit (QIAGEN, Inc.). This kit enabled the simultaneous purification of 96 samples in a 96-well block using multi-channel reagent dispensers. The recommended protocol was employed except for the following changes: 1) the bacteria were cultured in 1 ml of sterile Terrific Broth (Life Technologies) with carbenicillin at 25 mg/L and glycerol at 0.4%; 2) after inoculation, the cultures were incubated for 19 hours and at the end of incubation, the cells were lysed with 0.3 ml of lysis buffer; and 3) following isopropanol precipitation, the plasmid DNA pellet was resuspended in 0.1 ml of distilled water. After the last step in the protocol, samples were transferred to a 96-well block for storage at 4°C.

The cDNAs were sequenced by the method of Sanger et al. (1975, J. Mol. Biol. 94:441f), using a Micro Lab 2200 (Hamilton, Reno NV) in combination with PTC200 from MJ Research. and ABI 377 DNA sequencing systems (Perkin Elmer); and the reading frame was determined.

III Homology Searching of cDNA Clones and Their Deduced Proteins

The nucleotide sequences and/or amino acid sequences of the Sequence Listing were used to query sequences in the GenBank, SwissProt, BLOCKS, and Pima II databases. These

databases, which contain previously identified and annotated sequences, were searched for regions of homology using BLAST, which stands for Basic Local Alignment Search Tool (Altschul, S.F. (1993) J. Mol. Evol 36:290-300; Altschul, et al. (1990) J. Mol. Biol. 215:403-410).

5 BLAST produced alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST was especially useful in determining exact matches or in identifying homologs which may be of prokaryotic (bacterial) or eukaryotic (animal, fungal, or plant) origin. Other algorithms such as the one described in Smith, T. et al. (1992, Protein Engineering 5:35-51), incorporated
10 herein by reference, could have been used when dealing with primary sequence patterns and secondary structure gap penalties. The sequences disclosed in this application have lengths of at least 49 nucleotides, and no more than 12% uncalled bases (where N is recorded rather than A, C, G, or T).

The BLAST approach searched for matches between a query sequence and a database
15 sequence. BLAST evaluated the statistical significance of any matches found, and reported only those matches that satisfy the user-selected threshold of significance. In this application, threshold was set at 10^{-25} for nucleotides and 10^{-14} for peptides.

Incyte nucleotide sequences were searched against the GenBank databases for primate (pri), rodent (rod), and other mammalian sequences (mam); and deduced amino acid
20 sequences from the same clones were then searched against GenBank functional protein databases, mammalian (mamp), vertebrate (vrtp), and eukaryote (cukp) for homology.

IV Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on
25 which RNAs from a particular cell type or tissue have been bound (Sambrook et al., supra).

Analogous computer techniques use BLAST to search for identical or related molecules in nucleotide databases such as GenBank or the LIFESEQ database (Incyte Pharmaceuticals). This analysis is much faster than multiple, membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to
30 determine whether any particular match is categorized as exact or homologous.

The basis of the search is the product score which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1-2% error; and at 70, the match will be exact. Homologous molecules are usually identified by selecting those which show product scores between 15 and 40, although
5 lower scores may identify related molecules.

The results of northern analysis are reported as a list of libraries in which the transcript encoding HRM occurs. Abundance and percent abundance are also reported. Abundance directly reflects the number of times a particular transcript is represented in a cDNA library, and percent abundance is abundance divided by the total number of sequences
10 examined in the cDNA library.

V Extension of HRM Encoding Polynucleotides

The nucleic acid sequence of an Incyte Clone disclosed in the Sequence Listing was used to design oligonucleotide primers for extending a partial nucleotide sequence to full length. One primer was synthesized to initiate extension in the antisense direction, and the
15 other was synthesized to extend sequence in the sense direction. Primers were used to facilitate the extension of the known sequence "outward" generating amplicons containing new, unknown nucleotide sequence for the region of interest. The initial primers were designed from the cDNA using OLIGO 4.06 (National Biosciences), or another appropriate program, to be about 22 to about 30 nucleotides in length, to have a GC content of 50% or
20 more, and to anneal to the target sequence at temperatures of about 68° to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries (Life Technologies) were used to extend the sequence. If more than one extension is necessary or desired, additional sets of primers are designed to
25 further extend the known region.

High fidelity amplification was obtained by following the instructions for the XL-PCR kit (Perkin Elmer) and thoroughly mixing the enzyme and reaction mix. Beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, PCR was performed using the PTC200 (MJ Research) and the following parameters: Step 1,
30 94° C for 1 min (initial denaturation); Step 2, 65° C for 1 min; Step 3, 68° C for 6 min; Step 4, 94° C for 15 sec; Step 5, 65° C for 1 min; Step 6, 68° C for 7 min; Step 7, for 15 additional cycles; Step 8, 94° C for 15 sec; Step 9, 65° C for 1 min; Step 10, 68° C for 7:15 min; Step

11, Repeat step 8-10 for 12 cycles; Step 12, 72° C for 8 min; and Step 13, hold at 4° C.

A 5-10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were

5 excised from the gel, purified using QIAQUICK kit (QIAGEN Inc.), and trimmed of overhangs using Klenow enzyme to facilitate religation and cloning.

After ethanol precipitation, the products were redissolved in 13 μ l of ligation buffer, 1 μ l T4-DNA ligase (15 units) and 1 μ l T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2-3 hours or overnight at 16° C. Competent *E. coli*
10 cells (in 40 μ l of appropriate media) were transformed with 3 μ l of ligation mixture and cultured in 80 μ l of SOC medium (Sambrook et al., supra). After incubation for one hour at 37° C, the *E. coli* mixture was plated on Luria Bertani (LB)-agar (Sambrook et al., supra) containing 2x Carb. The following day, several colonies were randomly picked from each plate and cultured in 150 μ l of liquid LB/2x Carb medium placed in an individual well of an
15 appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 μ l of each overnight culture was transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 μ l of each sample was transferred into a PCR array.

For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer, and one or both of the gene specific primers
20 used for the extension reaction were added to each well. Amplification was performed using the following conditions: Step 1, 94° C for 60 sec; Step 2, 94° C for 20 sec; Step 3, 55° C for 30 sec; Step 4, 72° C for 90 sec; Step 5, Repeat steps 2-4 for an additional 29 cycles; Step 6, 72° C for 180 sec; and Step 7, hold at 4° C.

Aliquots of the PCR reactions were run on agarose gels together with molecular
25 weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid, and sequenced.

In like manner, the nucleotide sequence of SEQ ID NOs:11-20 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for 5' extension, and an appropriate genomic library.

30 VI Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NOs:11-20 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of

about 20 base-pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 (National Biosciences), labeled by combining 50 pmol of each oligomer and 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia) and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified with SEPHADEX G-25 superfine resin column (Amersham Pharmacia). A aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases (Asc I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II; DuPont NEN).

The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR film (Eastman Kodak, Rochester NY) is exposed to the blots in a Phosphorimager cassette (Molecular Dynamics, Sunnyvale CA) for several hours, hybridization patterns are compared visually.

VII Microarrays

To produce oligonucleotides for a microarray, SEQ ID NOs: 11-20 are examined using a computer algorithm which starts at the 3' end of the nucleotide sequence. The algorithm identified oligomers of defined length that are unique to the gene, have a GC content within a range suitable for hybridization, and lack predicted secondary structure that would interfere with hybridization. The algorithm identifies approximately 20 sequence-specific oligonucleotides of 20 nucleotides in length (20-mers). A matched set of oligonucleotides are created in which one nucleotide in the center of each sequence is altered. This process is repeated for each gene in the microarray, and double sets of twenty 20 mers are synthesized and arranged on the surface of the silicon chip using a light-directed chemical process (Chee, M. et al., PCT/WO95/11995, incorporated herein by reference).

In the alternative, a chemical coupling procedure and an ink jet device are used to synthesize oligomers on the surface of a substrate (Baldeschweiler, J.D. et al., PCT/WO95/25116, incorporated herein by reference). In another alternative, a "gridded" array analogous to a dot (or slot) blot is used to arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a vacuum system, thermal, UV,

mechanical or chemical bonding procedures. A typical array may be produced by hand or using available materials and machines and contain grids of 8 dots, 24 dots, 96 dots, 384 dots, 1536 dots or 6144 dots. After hybridization, the microarray is washed to remove nonhybridized probes, and a scanner is used to determine the levels and patterns of fluorescence. The scanned image is examined to determine degree of complementarity and the relative abundance/expression level of each oligonucleotide sequence in the microarray.

VIII Complementary Polynucleotides

Sequence complementary to the sequence encoding HRM, or any part thereof, is used to detect, decrease or inhibit expression of naturally occurring HRM. Although use of oligonucleotides comprising from about 15 to about 30 base-pairs is described, essentially the same procedure is used with smaller or larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software and the coding sequence of HRM, SEQ ID NOs:11-20. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the transcript encoding HRM.

IX Expression of HRM

Expression of HRM is accomplished by subcloning the cDNAs into appropriate vectors and transforming the vectors into host cells. In this case, the cloning vector is also used to express HRM in *E. coli*. Upstream of the cloning site, this vector contains a promoter for β -galactosidase, followed by sequence containing the amino-terminal Met, and the subsequent seven residues of β -galactosidase. Immediately following these eight residues is a bacteriophage promoter useful for transcription and a linker containing a number of unique restriction sites.

Induction of an isolated, transformed bacterial strain with IPTG using standard methods produces a fusion protein which consists of the first eight residues of β -galactosidase, about 5 to 15 residues of linker, and the full length protein. The signal residues direct the secretion of HRM into the bacterial growth media which can be used directly in the following assay for activity.

X Demonstration of HRM Activity

HRM can be expressed in a mammalian cell line such as DLD-1 or HCT116 (ATCC) by transforming the cells with a eukaryotic expression vector encoding HRM. Eukaryotic

expression vectors are commercially available and the techniques to introduce them into cells are well known to those skilled in the art. The effect of HRM on cell morphology may be visualized by microscopy; the effect on cell growth may be determined by measuring cell doubling-time; and the effect on tumorigenicity may be assessed by the ability of transformed
5 cells to grow in a soft agar growth assay (Grodin, J. et al. (1995) Cancer Res. 55:1531-1539).

XI Production of HRM Specific Antibodies

HRM that is substantially purified using PAGE electrophoresis (Sambrook, supra), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols. The amino acid sequence deduced from SEQ ID NOs: 11-20 is analyzed
10 using LASERGENE software (DNASTAR Inc) to determine regions of high immunogenicity and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions, is described by Ausubel et al. (supra), and others.

Typically, the oligopeptides are 15 residues in length, synthesized using an Applied
15 Biosystems Peptide Synthesizer Model 431A using fmoc-chemistry, and coupled to keyhole limpet hemocyanin (KLH, Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS; Ausubel et al., supra). Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity, for example, by binding the peptide to plastic,
20 blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radioiodinated, goat anti-rabbit IgG.

XII Purification of Naturally Occurring HRM Using Specific Antibodies

Naturally occurring or recombinant HRM is substantially purified by immunoaffinity chromatography using antibodies specific for HRM. An immunoaffinity column is
25 constructed by covalently coupling HRM antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing HRM is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of HRM (e.g., high ionic
30 strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/protein binding (eg, a buffer of pH 2-3 or a high concentration of a chaotrope, such as urea or thiocyanate ion), and HRM is collected.

XIII Identification of Molecules Which Interact with HRM

HRM or biologically active fragments thereof are labeled with ^{125}I Bolton-Hunter reagent (Bolton et al. (1973) Biochem. J. 133: 529). Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled HRM, washed and any wells with labeled HRM complex are assayed. Data obtained using different concentrations of HRM are used to calculate values for the number, affinity, and association of HRM with the candidate molecules.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

What is claimed is:

1. A substantially purified human regulatory molecule (HRM) comprising a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NOs:1-10.
- 5 2. An isolated and purified polynucleotide sequence having a nucleic acid sequence encoding the human regulatory molecule of claim 1.
3. An isolated and purified polynucleotide sequence which hybridizes under stringent conditions to the polynucleotide sequence of claim 2.
4. A composition comprising the polynucleotide sequence of claim 2.
- 10 5. An isolated and purified polynucleotide sequence having a nucleic acid sequence selected from the group consisting of: SEQ ID NOs:11-20.
6. A microarray containing at least a fragment of at least one of the polynucleotides encoding a polypeptide having an amino acid sequence having the sequence selected from the group consisting of SEQ ID NOs:1-10.
- 15 7. A microarray containing at least a fragment of at least one of the polynucleotides having a nucleic acid selected from the group consisting of:SEQ ID NOs:11-20.
8. An isolated and purified polynucleotide having a nucleic acid sequence which is complementary to the nucleic acid sequence of the polynucleotide of claim 5.
- 20 9. A composition comprising the polynucleotide of claim 5.
10. An expression vector containing the polynucleotide of claim 2.
11. A host cell containing the vector of claim 10.
12. A method for producing a polypeptide encoding a human regulatory molecule, the method comprising the steps of:
 - 25 a) culturing the host cell of claim 11 under conditions suitable for the expression of the polypeptide; and
 - b) recovering the polypeptide from the host cell culture.
13. A pharmaceutical composition comprising a substantially purified human regulatory molecule of claim 1 in conjunction with a suitable pharmaceutical carrier.
- 30 14. A purified antibody which binds specifically to the human regulatory molecule of claim 1.
15. A purified agonist which modulates the activity of the human regulatory

molecule of claim 1.

16. A purified antagonist which decreases the effect of the human regulatory molecule of claim 1.

17. A method for stimulating cell proliferation comprising administering to a cell
5 an effective amount of the human regulatory molecule of claim 1.

18. A method for preventing a cancer comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 13.

19. A method for treating or preventing a cancer comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 16.

10 20. A method for treating or preventing an immune response comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 16.

21. A method for detecting a polynucleotide encoding a human regulatory molecule in a biological sample, the method comprising the steps of:

15 a) hybridizing the polynucleotide of claim 8 to nucleic acid material of a biological sample, thereby forming a hybridization complex; and

b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide encoding a human regulatory molecule in the biological sample.

20 22. A method for detecting expression levels of polynucleotides encoding a human regulatory molecule in a biological sample, the method comprising the steps of:

a) hybridizing the microarray of claim 6 to labeled complementary polynucleotides derived from the biological sample, thereby forming hybridization complexes; and

25 b) determining expression of polynucleotides encoding a human regulatory molecule in the biological sample by identifying the presence of the hybridization complexes.

23. A method for detecting expression levels of polynucleotides encoding a human regulatory molecule in a biological sample, the method comprising the steps of:

30 a) hybridizing the microarray of claim 7 to labeled complementary polynucleotides derived from the biological sample, thereby forming hybridization complexes; and

b) determining expression of polynucleotides encoding a human regulatory molecule in the biological sample by identifying the presence of the hybridization complexes.

24. The method of claim 22, wherein before hybridization, the nucleic acid
5 material of the biological sample is amplified and labeled by the polymerase chain reaction.

<110> INCYTE PHARMACEUTICALS, INC.
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 HILLMAN, Jennifer L.
 BANDMAN, Olga
 SHAH, Purvi
 AU-YOUNG, Janice
 YUE, Henry
 GUEGLER, Karl J.

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<130> PF-0356 PCT

<140> To Be Assigned
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<150> US 08/933,750
 <151> 1997-09-23

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 Gly Thr Lys Gln Leu Lys Leu Asp Pro Ser Ile Phe Glu Ser Leu
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 Thr Glu Phe Asp Leu Glu Ala Glu Glu Tyr Val Pro Leu Pro Lys

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His Asp Leu Asp	Val Ala Asn Ala Arg	Pro Gln Gly Gly Gln	Asp		
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	260		265		270
Ile Thr Asp Lys	Leu Arg Gly Glu Ile	Asn Lys Val Val Asn	Lys		
	275		280		285
Tyr Ile Asp Gln	Gly Ile Ala Glu Leu	Val Pro Gly Val Leu	Phe		
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Val Asp Glu Val	His Met Leu Asp Ile	Glu Cys Phe Thr Tyr	Leu		
	305		310		315
His Arg Ala Leu	Glu Ser Ser Ile Ala	Pro Ile Val Ile Phe	Ala		
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Ser Asn Arg Gly	Asn Cys Val Ile Arg	Gly Thr Glu Asp Ile	Thr		
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Ser Pro His Gly	Ile Pro Leu Asp Leu	Leu Asp Arg Val Met	Ile		
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Ile Arg Thr Met	Leu Tyr Thr Pro Gln	Glu Met Lys Gln Ile	Ile		
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Lys Ile Arg Ala	Gln Thr Glu Gly Ile	Asn Ile Ser Glu Glu	Ala		
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Leu Asn His Leu	Gly Glu Ile Gly Thr	Lys Thr Thr Leu Arg	Tyr		
	395		400		405
Ser Val Gln Leu	Leu Thr Pro Ala Asn	Leu Leu Ala Lys Ile	Asn		
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Gly Lys Asp Ser	Ile Glu Lys Glu His	Val Glu Glu Ile Ser	Glu		
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 Asp Thr Ser Gly Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile
 65 70 75
 Phe Trp Met Ala Ala Pro Lys Asn Arg Arg Thr Ile Glu Val Asn
 80 85 90
 Arg Cys Arg Arg Arg Asn Pro Gln Lys Leu Ile Lys Val Lys Asn
 95 100 105
 Asn Ile Asp Val Cys Pro Glu Cys Gly His Leu Lys Gln Lys His
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 Glu Ile Arg Arg Gln Ile Gly Lys Gln Glu Gly Gly Pro Phe Lys

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 35 40 45
 Thr Arg Ile Gly Val Ala Val Asn Gly Val Arg Lys His Cys Ser
 50 55 60
 Asp Lys Glu Val Val Ser Leu Ala Lys Val Leu Ile Lys Asn Trp
 65 70 75
 Lys Arg Leu Leu Asp Ser Pro Gly Pro Pro Lys Gly Glu Lys Gly
 80 85 90
 Glu Glu Arg Glu Lys Ala Lys Lys Lys Glu Lys Gly Leu Glu Cys
 95 100 105
 Ser Asp Trp Lys Pro Glu Ala Gly Leu Ser Pro Pro Arg Lys Lys
 110 115 120
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 125 130 135
 Ser Ala Ser Ser Ser Pro Lys Arg Pro Ser Val Glu Arg Ser Asn
 140 145 150
 Ser Ser Lys Ser Lys Ala Glu Ser Pro Lys Thr Pro Ser Ser Pro
 155 160 165
 Leu Thr Pro Thr Phe Ala Ser Ser Met Cys Leu Leu Ala Pro Cys
 170 175 180
 Tyr Leu Thr Gly Asp Ser Val Arg Asp Lys Cys Val Glu Met Leu
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 Ser Ala Ala Leu Lys Ala Asp Asp Asp Tyr Lys Asp Tyr Gly Val
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 Glu Leu Lys Ser Thr Asp Met Lys Tyr Arg Asn Arg Val Arg Ser
 230 235 240
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 Asn Val Leu Ser Gly Ala Ile Ser Ala Gly Leu Ile Ala Lys Met
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 275 280 285
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 290 295 300
 Gly Gly Thr Thr Thr Asp Leu Phe Gln Cys Ser Lys Cys Lys Lys
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 Leu Leu Gly Ala Leu Pro Leu Arg Ser Leu Thr Arg Gln Leu Val
 50 55 60
 Gln Asp Glu Asn Val Arg Gly Val Ile Thr Met Asn Glu Glu Tyr
 65 70 75
 Glu Thr Arg Phe Leu Cys Asn Ser Ser Gln Glu Trp Lys Arg Leu
 80 85 90
 Gly Val Glu Gln Leu Arg Leu Ser Thr Val Asp Met Thr Gly Ile
 95 100 105
 Pro Thr Leu Asp Asn Leu Gln Lys Gly Val Gln Phe Ala Leu Lys
 110 115 120
 Tyr Gln Ser Leu Gly Gln Cys Val Tyr Val His Cys Lys Ala Gly
 125 130 135
 Arg Ser Arg Ser Ala Thr Met Val Ala Ala Tyr Leu Ile Gln Val
 140 145 150
 His Lys Trp Ser Pro Glu Glu Ala Val Arg Ala Ile Ala Lys Ile
 155 160 165
 Arg Ser Tyr Ile His Ile Arg Pro Gly Gln Leu Asp Val Leu Lys
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Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala	90
80	85
His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn	105
95	100
Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu	120
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Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu	135
125	130
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Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala	210
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Arg Gly Gln Thr Gly His Phe Glu Gly Ser Gly His Gly Ser Trp
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Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe Asn Lys Glu Leu
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Phe Leu Gln Ala Asn Cys Gln Phe Val Val Ser Glu Asp Gln Asp
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Tyr Thr Ala His Phe Ala Asp Pro Asp Thr Leu Val Asn Trp Asp

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Asn Ser Tyr Thr	1070	Cys Ser Ser Asp Ser	1075	Ala Leu Gly Pro Thr	1080
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Asn Ser Leu Val	Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser	740	745	750
Asp Asn Ser Asp	Arg Val Pro Val Pro Ser Phe Gln Asn Ser Phe	755	760	765
Ser Gln Ala Ile	Glu Ala Ala Phe Met Lys Leu Asp Thr Pro Ala	770	775	780
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 50 55 60
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 Thr Phe Arg Val Thr Val Gly Asp Ile Thr Cys Thr Gly Glu Gly
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 Thr Ser Lys Lys Leu Ala Lys His Arg Ala Ala Glu Ala Ala Ile
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 Pro Leu Met Pro Asp Pro Ser Lys Gln Pro Lys Asn Gln Leu Asn
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 170 175 180
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 Arg Glu Tyr Thr Thr Ile Cys Arg Leu Glu Ser Phe Met Glu Thr
 200 205 210
 Gly Lys Gly Ala Ser Lys Lys Gln Ala Lys Arg Asn Ala Ala Glu
 215 220 225
 Lys Phe Leu Ala Lys Phe Ser Asn Ile Ser Pro Glu Asn His Ile
 230 235 240
 Ser Leu Thr Asn Val Val Gly His Ser Leu Gly Cys Thr Trp His
 245 250 255
 Ser Leu Arg Asn Ser Pro Gly Glu Lys Ile Asn Leu Leu Lys Arg

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	290	295	300
Asp Glu Leu Ser	Ala Asn Gly Gln Tyr Gln Cys Leu Ala Glu Leu		
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Ser Thr Ser Pro	Ile Thr Val Cys His Gly Ser Gly Ile Ser Cys		
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 <213> Homo sapiens

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 Arg Leu Ala Leu Ser Gln Asn Gln Gln Ser Ser Gly Ala Ala Gly
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 Pro Thr Gly Lys Asn Glu Glu Lys Ile Gln Val Leu Thr Asp Lys
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 Lys Glu Glu Arg Glu Leu Leu Arg Ser Thr Thr Ser Thr Ile Glu
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 Gly Ala Phe Leu Ile Val Gly Asp Ala Gln Ser Arg Val Asp Asp
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 His Leu Met Gly Lys Gln His Met Gly Tyr Ala Lys Ile Lys Ala
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 Pro Asp Arg Asp Glu Arg Leu Lys Lys Glu Lys Gln Glu Arg Glu
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Tyr Lys His Arg	Ser Lys Ser Arg Asp	Arg Glu Gln Asp Arg	Lys		
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Val Lys Ser Gly	Ser Arg Glu Lys Gln	Ser Glu Asp Thr Asn	Thr		
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<212> DNA
<213> Homo sapiens

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<212> DNA

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<221> unsure

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<223> a or g or c or t, unknown, or other

<220> -

<223> 1568361

<400> 15

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<212> DNA
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47, C12N 15/70, 1/21, A61K 38/17, C07K 16/18, C12Q 1/68	A3	(11) International Publication Number: WO 99/15658 (43) International Publication Date: 1 April 1999 (01.04.99)
(21) International Application Number: PCT/US98/19839 (22) International Filing Date: 22 September 1998 (22.09.98) (30) Priority Data: 08/933,750 23 September 1997 (23.09.97) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 08/933,750 (CIP) Filed on 23 September 1997 (23.09.97) (71) Applicant (for all designated States except US): INCYTE PHARMACEUTICALS, INC. [US/US]; 3174 Porter Drive, Palo Alto, CA 94304 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LAL, Preeti [IN/US]; 2382 Lass Drive, Santa Clara, CA 95054 (US). HILLMAN, Jennifer, L. [US/US]; 230 Monroc Drive #12, Mountain View, CA 94040 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Mountain View, CA 94043 (US). SHAH, Purvi [IN/US]; 1608 Queen Charlotte Drive #5, Sunnyvale, CA 94087 (US). AU-YOUNG, Janice [US/US]; 1419 Kains		Avenue, Berkeley, CA 94702 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). GUEGLER, Karl, J. [CH/US]; 1048 Oakland Avenue, Menlo Park, CA 94025 (US). (74) Agents: BILLINGS, Lucy, J. et al.; Incyte Pharmaceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 10 June 1999 (10.06.99)
(54) Title: HUMAN REGULATORY MOLECULES (57) Abstract The invention provides human regulatory molecules and polynucleotides (collectively designated HRM) which identify and encode them. The invention also provides expression vectors, host cells, agonists, antibodies and antagonists. The invention further provides methods for diagnosing, preventing, and treating disorders associated with expression of human regulatory molecules.		

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DK	Denmark	LR	Liberia	SE	Sweden		
EE	Estonia			SG	Singapore		

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/12 C07K14/47 C12N15/70 C12N1/21 A61K38/17 C07K16/18 C12Q1/68		International Application No PC1/US 98/19839
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C12N C07K A61K C12Q Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MASATO KANEMAKI ET AL.: "Molecular cloning of a rat 49-kDa TBP-interacting protein (TIP49) that is highly homologous to the bacterial RuvB" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 235, no. 1, 9 June 1997, pages 64-68, XP002088338 ORLANDO, FL US see abstract see page 65, left-hand column, paragraph 6 - page 68, left-hand column, paragraph 1; figure 1 -----	1-14, 17, 18, 21-24
<input type="checkbox"/> Further documents are listed in the continuation of box C. <input type="checkbox"/> Patent family members are listed in annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "Z" document member of the same patent family		
Date of the actual completion of the international search 17 December 1998		Date of mailing of the international search report 03.05.99
Name and mailing address of the ISA European Patent Office, P.O. 2915 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer MONTERO LOPEZ B.

INTERNATIONAL SEARCH REPORT

national application No.

PCT/US 98/ 19839

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Please see Further Information sheet enclosed.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

Please see Further Information sheet enclosed.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please see additional sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1-24 partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:1, polynucleotide comprising SEQ ID NO:11 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:11; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

2. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:2, polynucleotide comprising SEQ ID NO:12 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:12; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

3. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:3, polynucleotide comprising SEQ ID NO:13 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:13; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

4. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:4, polynucleotide comprising SEQ ID NO:14 encoding the

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:14; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

5. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:5, polynucleotide comprising SEQ ID NO:15 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:15; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

6. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:6, polynucleotide comprising SEQ ID NO:16 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:16; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

7. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:7, polynucleotide comprising SEQ ID NO:17 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:17; vector and host cell comprising the polynucleotides and use thereof to produce

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

the polypeptide; agonists and antagonists of the polypeptide; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

8. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:8, polynucleotide comprising SEQ ID NO:18 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:18; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptides; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

9. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:9, polynucleotide comprising SEQ ID NO:19 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:19; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptide; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

10. Claims: Partially 1-24

Human regulatory molecule comprising SEQ ID NO:10, polynucleotide comprising SEQ ID NO:20 encoding the polypeptide, polynucleotides hybridizing therewith or complementary thereto; microarray containing a fragment of a polynucleotide of SEQ ID NO:20; vector and host cell comprising the polynucleotides and use thereof to produce the polypeptide; agonists and antagonists of the polypeptide; pharmaceutical composition comprising the human regulatory protein and antibody binding the same; use thereof in stimulating cell proliferation and preventing

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

cancer; use of the polynucleotides an microarray for detecting expression levels of polynucleotides encoding a human regulatory molecule.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 206

Although claim 17, as far as concerning an in vivo method, and claim 18 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

Further defect(s) under Article 17(2)(a):

Claims Nos.: 15, 16, 19, 20

Claims 15, 16, 19 and 20, referring to agonists and antagonists have not been searched due to the lack of technical description therefore.